IN THE CLAIMS

1. (currently amended) A method for diagnosing prostate cancer, the method comprising the step of detecting the presence or absence of an expression product of a human endogenous MMTV-like subgroup 2 (HML-2) ~~HML-2 endogenous~~ retrovirus in a patient sample.

2. (currently amended) The method of claim 1[[,]] wherein the expression product is ~~a~~ an RNA or a polypeptide.

3. (currently amended) The method of claim 1 ~~any preceding claim,~~ wherein the patient sample is a prostate sample or a blood sample.

4. (currently amended) The method of claim 1 ~~any preceding claim,~~ wherein the expression product is an [[a]] RNA comprising SEQ ID NO:155 ~~having the following formula: N_1-N_2-N_3-N_4-N_5-polyA, wherein:~~

~~N_1 is selected from the group consisting of: a sequence having at least 75% identity to SEQ ID NO:155, a sequence having at least 50% identity to SEQ ID NO:155 and that is expressed at least 1.5 fold higher relative to expression in a normal (i.e., non-cancerous) cell with at least a 95% confidence level, a sequence having at least 80% identity to at least a 20 contiguous nucleotide fragment of SEQ ID NO:155, and a sequence having at least 80% identity to at least a 20 contiguous nucleotide fragment of SEQ ID NO:155 and that is expressed at least 1.5 fold higher relative to expression in a normal (i.e., non cancerous) cell with at least a 95% confidence level;~~

~~N_2 is selected from the group consisting of: a sequence having at least 75% sequence identity to SEQ ID NO:156, a sequence having at least 50% identity to SEQ ID NO:156 and that is expressed at least 1.5 fold higher relative to expression in a normal (i.e., non~~

~~cancerous) cell with at least a 95% confidence level, a sequence having at least 80% identity to at least a 20 contiguous nucleotide fragment of SEQ ID NO:156, and a sequence having at least 80% identity to at least a 20 contiguous nucleotide fragment of SEQ ID NO:156 and that is expressed at least 1.5 fold higher relative to expression in a normal (i.e., non cancerous) cell with at least a 95% confidence level;~~

~~N_3 is selected from the group consisting of: a sequence having at least 75% sequence identity to SEQ ID NO:6, a sequence having at least 50% identity to SEQ ID NO:6 and that is expressed at least 1.5 fold higher relative to expression in a normal (i.e., non cancerous) cell with at least a 95% confidence level, a sequence having at least 80% identity to at least a 20 contiguous nucleotide fragment of SEQ ID NO:6; and a sequence having at least 80% identity to at least a 20 contiguous nucleotide fragment of SEQ ID NO:6 and that is expressed at least 1.5 fold higher relative to expression in a normal (i.e., non cancerous) cell with at least a 95% confidence level;~~

~~N_4 comprises any RNA sequence;~~

~~N_5 is selected from the group consisting of: a sequence having at least 75% sequence identity to SEQ ID NO:5, a sequence having at least 50% identity to SEQ ID NO:5 and that is expressed at least 1.5 fold higher relative to expression in a normal (i.e., non cancerous) cell with at least a 95% confidence level, a sequence having at least 80% identity to at least a 20 contiguous nucleotide fragment of SEQ ID NO:5, and a sequence having at least 80% identity to at least a 20 contiguous fragment of SEQ ID NO:5 and that is expressed at least 1.5 fold higher relative to expression in a normal (i.e., non cancerous) cell with at least a 95% confidence level; wherein at least one of N_1 or N_5 is present, but N_2, N_3, N_4 and polyA are optional~~.

5. (currently amended) The method of claim 4[[,]] wherein the expression product is an RNA comprising SEQ ID NO:5 ~~comprises N_1~~.

6. (currently amended) The method of claim 4 [[5,]] wherein SEQ ID NO:155 ~~N_1~~ is at the 5′ end of the RNA.

7. (currently amended) The method of claim 1 [[4,]] wherein the RNA comprises SEQ ID NO:155 and SEQ ID NO:5 ~~N_4 comprises a polypeptide coding sequence~~.

8. (canceled)

9. (currently amended) The method of claim 2 [[8,]] wherein the expression product is a polypeptide and wherein the polypeptide is selected from the group consisting of ~~mRNA encodes one or more of the following HML-2 polypeptides:~~ gag, prt, pol, env, cORF, and tat.

10. (currently amended) The method of ~~claim 8 or~~ claim 9[[,]] wherein the polypeptide is detected using an antibody.

11. (currently amended) The method of claim 1 further comprising the step of ~~A method for diagnosing prostate cancer, the method comprising the steps of: (a)~~ obtaining the ~~a~~ patient sample ~~containing prostate cells; and (b) detecting the presence or absence of an expression product of HML-2 endogenous retrovirus in the patient sample~~.

12. (canceled)

13. (currently amended) The method of claim 11 ~~or 12, wherein step (b) is preceded by a~~ further comprising the step of enriching RNA in the patient sample.

14. (currently amended) The method of claim 1 ~~any one of claims 1 to 6 or 11 to 13,~~ wherein the expression product is detected using PCR, SDA, SSSR, LCR, TMA or NASBA.

15. (currently amended) The method of claim 14[[,]] wherein the PCT is RT-PCR.

16-38. (canceled)